

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/42/, 106ASource: 1600Date Processed by STIC: 1/9/2003

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JAN 2 1 2003

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

TECH CENTER 1600/2900

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (http://www.uspto.gov/ebc/efs/downloads/documents.htm, EFS Submission User Manual/- ePAVE)
- 2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
- Hand Carry directly to:
 U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202

U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

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1600

TECH CENTER 1600/2900

RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003 TIME: 10:55:57

Corrected Diskette Needed

Input Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

2 <1105 AFFLICANT: Byram, Joseph R. 4 <12GS TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS pr 1-7 7 <130: FILE REFERENCE: 38-21(15598)B 3 <140 - CURRENT APPLICATION NUMBER: 09/421,106A 10 <141 CURRENT FILING DATE: 1999-10-15 12 - 150 - NUMBER OF SEQ ID NOS: 36938 Does Not Comply

ERRORED SEQUENCES

14 - 210 SEO ID NO: 1 15 - 311: BENGTE: 147 TYPE: DNA ORGANISM: O yeine max 19 CRES OTHER INFORMATION: unsure at all n locations E--> 20 <400> SEQUENCE: 1

22 actcattage ttatggagaa getttttett tttaactnte tteteetatt agagettata 24 quaangotta tomasamaay ggocactata tattotgcaa tetggtactg tgccatatat > **26 atggatggtg ghtttggaca tttggat** > 51 -00100 SEP 3D NO: -3 52 -02110 SENGTE: 423 So -00120 TYPE: DNA 54 KR13F OF GANISH: Glycine max) 22207 36 - 1223 OTHER INFORMATION: unsure at all n locations

E--> 57 <400> SEQUENCE: 3

59 agetigtgag tigtgagegy laccadugaa aataceeeca edataceece titedeetta. > 61 toacaaacta tgggaatac tattgctact ccagaacaat gatctttagt taatctacac 65 titangitaa ttoaatcatc taattacctt gcagacccta aaatcagaga agattgagtt 120 180 240 #5 tyttqtaght coalatgaag dagatgotoa gttagogtad atgtotoago ttggagtada 300 67 adatqqoqqa qtiqcaqeqq tgatcacaga agataqtqat ctaataqcat atgqctqtcc > 69 agetgtaaga acteeteeaa taetgtgata ttgegeatgg aggtttaetg qnnttttgat 360 71 a cheqatit athrachtqt toactattoa gottoataga aagoatgoat tttggggatat 4 ± 0 423

76 FB10: SEQ ID NO: 4 77 HE11: LENGTH: 462 78 - HIZE TYPE: DNA

79 - 213 - CEGANISM: Glycine max 81 +223> OTHER INFORMATION: unsure at all n locations

E--> 82 <400> SEQUENCE: 4

84 receatetgt tetttagerg tacaaaaaca caateeetat catggattaa cacategaga 86 greatitizing dealectering generality tighted etactiggest acategrated 120 88 aaacaqtaca qoaqatqaaa atqqtqqqto qoattaacot toacaatttq qoaqoacaqa -

240 300

3.50

420

464

RAW SEQUENCE LISTING PATE: 01/09/2003 PATENT APPLICATION: US/09/421,106A TIME: 10:55:57 Input Set : D:\SoyBac.txt Output Set: N:\CRF4\01092003\I421106A.raw 90 aatoggacta tittotoaaa cqaaccatti aatggaagca qaatgaatga gdatgcagtg -92 ttactqotot yqtratqqtt cacaqaqotq qaqaaaaqat ttacaqaqca ttacaactac > 94 tggtccagca acctatcagt agctntctgt aactagcata gatgggaagc tattgaccaa 360 96 atglaacaat glaictagic iggalictas cagagggacc licalcecac acagicalac 420 462 98 tectquatto thagtaccon agractitto tataatataa at 101 <213> SEQ 10 NO: 5 102 <211> LENGTH: 394 10 s k Mill PYPE: DNA - ORGANISM: Glycine max 166 G25 OTHER INFORMATION: unsure at all n locations E--> 107 <400> SEQUENCE: 5 109 agetityeet etiigaadaa atabeeetea geeaaataga atedatettg ggeettitte 11% chackantot cakaaliggg agagaaligt toatclaaag catacaagto cotaatatta 113 toasatoeta aaattigago tootagggag caaaaraatg tgtgthtoot agagagggoa 115 teadchacea carrightit heosititig tattigalaa caratggaaa tigetetagg 240 11% tantificación attitignatig cotottigget abottignite gonototaat glactiaagt. 300 119 participat cantaignat gacamattee tiggments goldtigem ectaeestte 360 ⊕ > 121 ngcgggaggg cgacgcgtga ctcgcgggat gcgt 394 194 83100 SEQ 10 NO: 6 135 3211: LENGTH: 464 116 (Cl. TYPE: CM. 127 KOIR DEGANISM: Glycine max 129 CO23: OTHER INFORMATION: unsure at all n locations E--> 130 <400> SEQUENCE: 6 🎢 > 132 ntaagaggat gctntaatgg agganaataa agagagaagg ngggagcaca aaattgaagg 60 1% hatawaatag gamgagaagt ggaacattga agtgtgtoto atawgwottt cattoatoaa 120 180 Tiff agtiaceans agrettaced atgettetat tietageche gghagnitod tigageagot



142 itertasaga agrisqaqri tagetacaba taceteteta utagetaage teaceteett 144 gagatgggaa gctagagctn tgctacacac ccnctatgat agctaagctc accccatga 146 caaaatacat ganaatacaa aaaagatccc tactacaaag acta 149 (210) SEQ ID NO: 7

13% treifgagga sauttuetig agaaacttot tigaaaaaac ficetigaga aggtagaget

14% tagetalada carceatoto ataactaago toacctorit gagaagittio cataagaaga

180 4211> LENGTH: 373 151 -02120 TYPE: DNF.

152 02139 OEGANISM: Glypine max) 2227
164 02230 OTHER INFORMATION: unsure at all n locations

E--> 155 <400> SEQUENCE: 7

189 teogetsage genabactea tiggetaage geaaggaaga atotggaaga aaatgagetg 120 180 161 madaagttog ottageadad tigtitogtot babtaagege abogottoag todatbaget. 163 Hagorabaaa gooboqoqot aagooqaaat toactaatgt gogotaagog gtocagaatt 240 165 degetalaging calegageling albaaggeea contattitaag offigalaatea gattitigitga 300 360 167 agggagttig gg::Laggatt cagagettig catgictaga gattetagag agagaaaggt 373 169 ocaatttoag aga

136 -0210> SEQ ID NO: 9 190 (211) LENGTH: 421 198 -01120 TYPE: DNA

199 <213> CRGANISM: Glycine max

RAW SEQUENCE LISTING

FATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003 TIME: 10:55:57

Input Set : D:\SoyBac.txt Output Set: N:\CRF4\01092003\I421106A.raw 201 <223> CIHER INFORMATION: unsure at all n locations E--> 202 <400> SEQUENCE: 9 204 agentitgadt itagteatea agagattata aanatgigad aatggdatga gittidaataa 206 taatcaataa totatoiitt adataatott ofifdaadad doitdaatda atottidaaf 208 alettettta areteritea acattileaa eagalettte igaltitalti eeettealet-240 210 ttotaaaagt tiitoikoaa täyttöötöt tooaagaaaa gitoittigit oaaaaaotto. 311 211 agetatteat etittieatt etetretece *ffqccaaaa qaaggaagga etaacegeet 360 214 gaattttttt gtgtctctct tctcccttac aaaagattca naggactaac cgcctgatat 216 atotittott toosoalaba aagatitaaa qyastaabig ootgagaatt oittytooba 4.30 4:1 218 a 2.4 <210> SEQ ID NO: 10 2. H <211> IENGIH: 404 ADD <2125 TYPE: DNA 2.54 K2135 CRGANISM: Clycine max) $\angle 2207$ z. + < > 2.27> OTHER INFORMATION: unsure at all n locations E--> 227 <400> SEQUENCE: 10 2.1. Laterigeost coesituasea gracetroat agraggigea ggaccateaa cagebageeg 23. bagatgeaco acciaecquet etacateago etropyteett agagtobate teageteaca. 1. 1 2... ccasteating additing the candidate adaptitude condition of the con 2% agagetagga theragoest tactogtgge thactedega glagtitiggg geoacagitig (*) (*) 2: + ratgacctig agutaggeod aattiticaag tagggacaag accetoaaag geodeaggag Sep. 🖔 241 ttgaagatgg agctcaagaa gacgacgaca tangcgatgt gatg 404 4 KIC SEQ ID NO: 13 valle LEMGTH: 334 🕠 KR120 TYPE: DNA 25% <213% ORGANISM: Glycine max \longrightarrow \angle 2 2 c \angle 2 · + < 23 : OTHER INFORMATION: unsure at all n locations E₇-> 290 <400> SEQUENCE: 13 24. agetigosto actitiaest titeatites alegiaetet igetisaaaa aeigsseaat 2.4 originaging tittingings calculational atcascatag typical typicasas -1.01> 296 aagattgete ttgeetttga etttetetat eteetetegn gatttttttt atttgageaa 29- begingstia teeggiaggg giggaacite gialaigiet ilaalaiett eesalagale. w--> 300 acaagcatca agatagggtt ccgttctaat agcctagagg tggtaatgtt ntccattgaa 300 333 2 . tagtijasaje otatigsagea oggacaceet agticeetta 3.7 kzio: **55**Q ID NO: 15 3. + KR110 LENGTH: 354 3. 3 <2120 TYPE: DNA 340 k2130 OEGANISM: Glydine max \longrightarrow \angle \angle \angle \bigcirc 34. K2239 OTHER INFORMATION: unsure at all n locations E--> 333 <400> SEQUENCE: 15 60 >, 335 agcttgcata actntgaatg gngtattggt agagtttatc cgttaatgat atgggctatt 337 gagttgggga ggattgattn tggaacttgt cgtggtgcag aagttagttc aagtgcgaac 120

3.) Actactagaa aanqaqettt ttgcgatgea ettacgacat eggteeaaca aaactgtega

34: agtafattsa atggtgdatt tgtgtaatta daadgaaagt gtgdaccttg ddaattttat

34% ggftqadatt qqds-maarto oottgaaggt tgttggaagg gadtogagag tgaggaaadt 34% agadagdtig qqqtattoto gatttoogta adatacttaa tgototbada adatagtgga 180

2:1

300

360

384

388 <210> SEQ ID NO: 18

E4T gitagggtag tamaitteac catt

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/421,106A

DATE: 01/09/2005 TIME: 10:55:57

Input Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

```
289 k 2115 LENGTH: 443
     390 <212; TYPE: DNA
     391 <213) CRGANISM: Glycine max → ∠∠207
     393 < 223% OTHER INFORMATION: unsure at all n locations
E--> 394 <400> SEQUENCE: 18
W--> 396 ctnggtgttg ttcctattgt gcgagttact gaggtgcaat ttcaatttta attggataat
     592 gagaaatgit agdastatad tarogtatga dactgoatda badactitat tattigodad
                                                                             120
     40% aantitatigg aaatbamaaa attiigigg tiotqttact tatttaatga acticabicg
    40. lgattttgga atttrialta aattttaacc aataataata ataatagagt gtgttarfta
   oldsymbol{igcup} 404 gangggraft gintigetag castrofett gangtatage atacaaacat ganaggantt
                                                                             300
  -> 406 ccattttaaq tattatcctq taccanaacc tcactttaqt ccccaatttt ggaaatcaca
                                                                            360
                                                                            420
W--> 408 gttcttttca ctgacaaatg acttacagtt ntagttaaaa atagggatta acaagagtgg
                                                                             4.13
    410 agbatacaag accasquigg act
     41% <210% SEQ ID NO: 10
     414 <211> IENGTE: 396
     415 <2125 TYPE: DNA
     416 - 2180 ERGANISM: G.yoine max 🛶 🚄 207
    415 (2.13) OTHER INFORMATION: unsure at all n locations
E--> 419 <400> SEQUENCE: 19
                                                                            en it
     45) agentitagen ggaetawaaa acantataan eechteaana ghaqgangag agnangeene
     40% timbagtatt tehtteaagt attgrighera khetagaaad aagaataaga gaaaattaaa.
    415 gggaatgbag tragtoubat garafatiga gattigtitt tittitotit tittigtaati
                                                                           180
    42\% garawasang schassarigg tigtictittig: aftawaggigd cittleagwag wactigtigal
     d≱n aarawattya towyttisat troottalac ticaaqigaa aagattitta tactaigaac
                                                                             300
WH-> 431 taaccaaaaa tcatcctatg attnttaata taattattat aaaattacca tacatcataa 360
                                                                             396
W--> 433 tttgagaatg tagaanacat aaacaacgtt tacact
    456 <2100 SEQ ID NO: .00
    437 k2110 femgre: 469
     456 <2120 TYPE: DNA
    E--> 442 <400> SEQUENCE: 20

ho_{/}444 gtcctcgggc cattcctgcg aaggaaaaca tttggatagt tagttntacc aagaaatgct
   \mathcal{L}_{446} acceptisada camada ggo atacadecto etecadatada tacadacato datgiadati.
     44) tamaqualago statgoquat attitictiae galacattoae togolacaaga tattotiota.
                                                                            180
     450 actiangassa atquaccoat geacaateaa ggeaettteg ttacetaeat taittgtatg 240
     48% tasticcang gigisciade tacabeacat gealticett gestaaatti abatacatge
    4\%4 atymicasag coloriquet accassaget gescattge sesettiatg atgestottg
                                                                             360
    45% got:stotada bahtaaqqtg otacacttca tgotttatat baagtgtttt actaccagaa.
                                                                            4.20
     45% geogratgeg satgtongta tattttettt tgeogacta
                                                                             459
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    461 <2110 LENGTH: 328
    468 <2130 TYPE: DNA
    464 <213> OEGANISM: G.ycine max _
    466 <223> OTHER INFORMATION: unsure at all m locations
E--> 467 <400> SEQUENCE: 21
    46^{\rm th} agettetede equatitiet atawataggg ggagaagtgt agtagawaag ggtteagted
    471 offaggeact referent tegesettige (taggeass) ightrengty asgassator
     475 aageogaqqe getteeqtaa egttteeqtg agtgatttig egaaggittit egacegitet.
```

DATE: 01/09/2003 TIME: 10:55:57

Input Set : D:\SoyBac.txt Cut put Set: N:\CRF4\01092003\I421106A.raw W--> 475 tegaegntet teattegtte tteategnte tteagtette aaegggtaag taceteatae $\mathbb{W}_{T}>477$ caagetttte aatteattet atataeeegn nnggggeeae attatggtte atgtattatt 479 attetegntt catttactet ttatacce 328 48.0 <210° SEO ID NO: 32 483 <211 - LEUGTH: 591 494 < 112 - TYPE: DNA 4-5 < 013 + OR ANISM: G. veine max __) 2 2 207 4ml <.23 OTHER INFORMATION: unsure at all n locations E--> 488 <400> SEQUENCE: 22 1/7/> 490 ggctctanat ntacattgat gtttgtattt atgggaggag gttatatgcc atttttgctt 4.00 transpagness groups migg talaalachaac ittecaalang titigeetteg eaggaatgde 120 474 diagraphs of each man against coap gaaggacaan geogrammas gaactantic. 18040% egeo-equig taccamigte accorditing gagestigta caccascass settessasse. 499 catruaggia tygtogrifte toogugagog acgegtocag etbatggaeg acgagtatae 500 tyasiteriy gaqqaallag ggegenggeg gtaggbacca tiggitacib chatggbbaa. 360 502 juituatora gadata picc tegagittea t 391 5.5 K. 10 SEP ID NO: 24 5. 6 K. 11 DENGTH: 438 % T K. 12 IYFE: DNA 5.8 < 13 - OFBANISM: Brycine max 2227 6.0 t.23 OTHER INFORMATION: unsure at all n locations E--> 531 <400> SEQUENCE: 24 が 533 ggcacactet ntgattatet tggtetacea agtgtttatt acacaatagt gaaatgeact 1995 tartifocalt biocusgoto appoactigaa togaattato tobagobabb caactacabb 1.20 m^{2} chasatagug gtilapadag gaadeadact aacaetgeca ataaccecaa gtimcaggit firm traphtoppa atratachat tathamang ggttotacaa octottatag aagbataach 541 ortgrassha otritsurag tasawangaa awaaaaaact ttaogtoaca gaactoacta 360 543 d Maddigawa maddiac mad mitglioggit itgtactotgo mgtotgomog tigtitochia. 145 aabaqaaana daribaritti aaattaatta atrgattaat actaocatca agtagtacca. 4.20 14% endomatant officiality 4.38 5-4 K. 10. SEG 10 NO: 27 585 < 11 - LENGTH: 373 FRG C 120- TYPE: DNA For C13 CEGANISM: Phycine max $\frac{2207}{1.00}$ C.23. CTHEE INFORMATION: unsure at all n locations E--> 590 <400> SEQUENCE: 27 W--> 592 agettetece ceaattntet ataaataggt ggagaagtga agtgaanaag ggtteageee inductionage and termination of the togalattic temperature togalatic temperature and the temperature of temperature of temperature of the temperature of temperature of temperature of t 1:20 Tim asgergagio gettoegaaa egitteegia aegitteegi gaggaattie gegaaggitti 180 Light equalified tequestred teattegite iteategite itegatetic adegggtaag -240Note: tracer egalar caracterite gatteattet atgtacetgt ggtggtecae attgtggtte. 300 \widetilde{W} --> 602 gtggattttt attotogntt catttacttt otataccocc ttttgacgtg gottaagoca 360 + P4 ittaittaag toattione 379 *19 < 100 SEQ ID NO: 29 esc <.10 LFNGTH: 405 6/1 < 10/ TYPE: DNA 6.2 < 13> ORGANISM: Glycine max) $\angle 2207$ 654 < 23> OTHER INFORMATION: unsure at all n locations

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/421,106A

E--> 635 <400> SEQUENCE: 29

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/421,106A

DATE: 01/09/2003 TIME: 10:55:57

lnput fet : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

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(K	<i>1</i> }/ ₇ >					caacccanaa			120	
W	1>	641	ntatctatga	actgtacaaa	atacacgact	cctcaattgt	tctcaaaata	attttatcta	180	
		642	allogogottg	tgattaaact	agtbaggtor	caacagtggt	toccatoata	atactogeca	240	
		645	egeattaact	agtagacatit.	agattcatag	ttcacaaatc	agggcacaca	adaticticaat	300	
		647	gcacatatat	attacaagtd	aatacatact	caatttatca	catacatttq	gteteaatea	3.60	
		649	cagtggtata	atctcaattt	aacatgttat	cacacct cat	gaatbata		4 O E	
			<2100 SEQ 0							
		655	<211: LENG	rH: 443						
			<212. TYPE		_	22 2				
		655	<2131 ORGAN	NISM: Glycin	ne max) <	12207				
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W	7>					acaagattac			60	
^	1 1					aaatcatgag			120	
	\sqrt{I}					aaabaaatgo			180	
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			-			atgetgttte			306	
	/0					aagtcataaa			360	
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				aaqqaataca	i cg				4.13	
			<210: SEQ :							
			<211: LENG!							
			42120 IYPE		;	100				
		-68G	<2131 ORGAI	NISM: Glynla	<u>. max)</u>	222				
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TIN

sel p.7 for more orion

09/421,106A 7

<210> <211> <212> <213>	36937 22 DNA Artificial Sequence
<400>	36937 Leg gatgettett et leg 22
gtgtctt	ecg gatgettett et
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caccattttg cacctaagtt ga



PATE: 01/09/2003 TIME: 10:57:26

RAW SEQUENCE LISTING ERROR SUMMARY
LATENT APPLICATION: US/09/421,106A

Input Set : D:\SoyBac.txt

Output Set: N:\CRF4\01092003\I421106A.raw

Use of <220> Feature(NEW RULES):

Sequence(s) __are missing the <220> Feature and associated headings. Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32) (Sec.1.823 of new Rules)

Seq#:36937,36938